SEQUENCE LISTING

<110> MBARI DeLong, Edward Beja, Oded <120> Light-driven energy generation using proteorhodopsin <130> MBA-101 <150> 60/201,602 2000-05-03 <170> PatentIn version 3.0 <210> 1 <211> 105184 <212> DNA <213> Naturally occurring gamma proteobacterium <220>

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  Hadd, A., Nguyen, L.P.,
                                   Jovanovich, S.B., Gates, C.M.,
  Feldman, R.A., DeLong, E.F
  <302> Bacterial rhodopsin: evidence for a new type of phototrophy in
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Ficta																432
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					ggt Gly											672

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Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu 120 125 115 Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp 160 145 150 155 Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys 165 170 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr 180 185 190 Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly 195 200 205 ũ Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr 220 210 215 Ì₽₽. Ш Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp **J** 225 235 240 230 🗖 Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250 245 <210> 6 <211> 747 <212> DNA <213> Naturally occurring gamma proteobacterium

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                                                                            96
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Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met Arg 65 70 75 80

Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr Ile 85 90 95

Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu Ile 100 105 110

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Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr

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10 May 1				20					25					30			
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Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

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					gtt Val												240
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den ipe gre hae je mil tim					gca Ala												384
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Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys 165 170 175

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Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr 210 215 220

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			gca Ala												576
			atc Ile 195				-								624
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Met Gly Lys Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr

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Ph Va 65 Ar II

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25

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 140

Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr 180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr

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220

215

60

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55

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					cct Pro						4	480
					cta Leu						į	528
					gtt Val						į	576
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Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Ala 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met 65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu 115 120 125

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				gta Val													480
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Ser	Phe	Trp 35	Leu	Val	Thr	Ala	Gly 40	Met	Leu	Ala	Ala	Thr 45	Val	Phe	Phe	
Phe	Val 50	Glu	Arg	Asp	Gln	Val 55	Ser	Ala	Lys	Trp	Lys 60	Thr	Ser	Leu	Thr	

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp Leu Tyr Met Ile Tyr Glu Leu His Met Gly Glu Gly Lys Ala Ala Val Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Lys Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala

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   Phe Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
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   tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt
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   Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
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                                40
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       50
                            55
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   gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg
   Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
                                                                 80
                                            75
   65
                       70
                                                                          288
   aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat
   Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
                                                             95
                   85
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Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Val Val Glu Phe Tyr Leu

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		gct Ala													480
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  Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
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                                               220
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  Phe Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
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												aaa Lys 60					192
												cat His					240
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	att Ile	gat Asp	tgg Trp	tta Leu 100	tta Leu	act Thr	gtt Val	cca Pro	tta Leu 105	caa Gln	atg Met	gtt Val	gag Glu	ttc Phe 110	tat Tyr	cta Leu	336
	Ile	ctt Leu	gct Ala 115	gct Ala	tgt Cys	aca Thr	aat Asn	gtt Val 120	gct Ala	gct Ala	tca Ser	tta Leu	ttt Phe 125	aag Lys	aag Lys	ctt Leu	384
	Leu	gct Ala 130	ggt Gly	tca Ser	tta Leu	gta Val	atg Met 135	tta Leu	ggt Gly	gct Ala	gga Gly	ttt Phe 140	gca Ala	ggc Gly	gaa Glu	gct Ala	432
	gga Gly 145	ttg Leu	gct Ala	cct Pro	gta Val	tgg Trp 150	cct Pro	gct Ala	ttc Phe	att Ile	att Ile 155	ggt Gly	atg Met	gct Ala	gga Gly	tgg Trp 160	480
•	tta	tac Tyr	atg Met	att Ile	tat Tyr 165	gag Glu	cta Leu	tat Tyr	atg Met	ggt Gly 170	gaa Glu	ggt Gly	aag Lys	gct Ala	gct Ala 175	gta Val	528
	agt Ser	act Thr	gca Ala	agt Ser 180	cct Pro	gct Ala	gtt Val	aac Asn	tct Ser 185	gca Ala	tac Tyr	aac Asn	gca Ala	atg Met 190	atg Met	gtg Val	576
	att Ile	att Ile	gtt Val 195	gtt Val	gga Gly	tgg Trp	gca Ala	att Ile 200	tat Tyr	cct Pro	gct Ala	gga Gly	tat Tyr 205	gct Ala	gct Ala	ggt Gly	624
	tac Tyr	cta Leu	atg Met	ggt Gly	ggc Gly	gaa Glu	ggt Gly	gta Val	tac Tyr	gct Ala	tca Ser	aac Asn	tta Leu	aac Asn	ctt Leu	ata Ile	672

720 tat aac ctt gcc gac ctt gtt aac aag att cta ttt ggt ttg atc att Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile 225 230 235 240 753 tgg aat gtt gct gtt aaa gaa tct tct aat gct Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250 245 <210> 23 <211> 251 <212> PRT <213> Naturally occurring gamma proteobacterium <400> 23 Met Gly Lys Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser 15 **I** 1 5 10 <u>|</u> ■ Phe Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val 30 20 25 Ш Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe 35 40 45 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met 75 80 65 70 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr 85 90 95 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu

220

215

210

Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala

Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val

■ Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile Uī

Figr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile **□**225

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			atg Met														528
			gca Ala														576
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Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 140

Gly Ile Met Asn Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys 165 170 175

Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala 180 185 190

Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr 210 215 220

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Phe Ala Ala Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
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                                25
                                                     30
                                                                      144
tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
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                                                 45
                                                                      192
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Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
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                                             60
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	_					gtt Val										336
						aat Asn										384
						atg Met 135										432
						ggt Gly										480
						ctt Leu		Leu								528
						gtt Val										576
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Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 140

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Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp
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145
                    150
Val Tyr Met Ile Tyr Glu Leu Trp Leu Gly Glu Gly Lys Ala Ala Cys
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                                     170
                                                          175
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Met
                                 185
            180
Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
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                                                  205
        195
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
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                         215
    210
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
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												cat His					24	40
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: Cl												tgt Cys					33	36
												ctg Leu					38	84
												tac Tyr 140					43	32
												ggg Gly					48	80
												ggc Gly					52	28
	aat	act	gca	agt	cct	gct	gtg	caa	tca	gct	tac	aac	aca	atg	atg	tat	5′	76

Asn	Thr	Ala	Ser 180	Pro	Ala	Val	Gln	Ser 185	Ala	Tyr	Asn	Thr	Met 190	Met	Tyr		
					tgg Trp	_				_						ı	624
		_			ggt Gly											(672
		-	_		gtt Val 230											,	720
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Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala

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                                 25
                                                     30
tct ttt tgg tta gtt aca gct gct cta tta gca tct act gta ttt ttc
                                                                       144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
                                                 45
        35
ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act
                                                                       192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
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                                             60
    50
                                                                       240
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Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
                                                             80
                                         75
                    70
65
aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac
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Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
                                                         95
                                     90
                85
                                                                       336
att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
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L

100

105

110

		_	-	-		aat Asn		-					384
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						cct Pro							480
_						cta Leu							528
						gtt Val							576
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						ggg Gly 215							672
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	_	_	_		_	tct Ser							750

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Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 140

Gln Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys 165 170 175

Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala 180 185 190

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Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
                        215
                                             220
    210
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Leu Gly Leu Ile Ile Trp
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Asn Val Ala Val Lys Glu Ser Ser Asn Ala
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Phe Ala Ala Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
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                                                                      144
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	_				_				_			cat His					240
												act Thr					288
		_					-					tgt Cys					336
			_	_	_	_		_	-			tta Leu					384
U H												tac Tyr 140					432
u			_	_	_			-				ggg Gly					480
	_		_			_			_		-	gga Gly					528
												aac Asn					576
												ggt Gly					624
												tta Leu 220					672
	aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggt	tta	att	ata	tgg	720

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Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp 225 230 235 240
```

aat gtt gct gtt aaa gaa tct tct aat gct Asn Val Ala Val Lys Glu Ser Ser Asn Ala 245 250 750

<210> 33

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 33

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr 1 5 10 15

Phe Ala Ala Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 85 90 . 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

<u>I</u>
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<u> </u>
13
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L

Ile Leu Ala Ala Ala Asn Val Ala Gly Ser Leu Phe Lys Lys Leu 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr 180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala 245 250

<210> 34

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB40m1; GenBank #AF349988

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		aaa Lys											48
		gca Ala											96
		tgg Trp 35											144
	_	gaa Glu	_	_	_	_							192
_		ggt Gly		-				_					240
_		gta Val			_			_	_				288
		tgg Trp											336
		gct Ala 115											384
		ggt Gly											432
		atg Met	_	_			_						480

	145					150					155					160		
	_		_			_					_	gga Gly					52	28
			-	_		_	_			_		aac Asn					5′	76
			_								-	ggt Gly					6:	24
												tta Leu 220					6'	72
												ggt Gly					7:	20
		_	_	gtt Val		_											7!	50
i Li	<210)> 3	35															
	<211	.> 2	250															
	<212	!> I	PRT															
	<213	> 1	Natui	rally	, oca	curri	ing g	gamma	a pro	oteok	oacte	eriun	n					
	<400)> 3	35															
	Met 1	Gly	Lys	Leu	Leu 5	Leu	Ile	Ile	Gly	Ser 10	Val	Ile	Ala	Leu	Pro 15	Thr		
	Phe	Ala	Ala	Gly 20	Gly	Gly	Asp	Leu	Asp 25	Ala	Ser	Asp	Tyr	Thr 30	Gly	Val		

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe

W

1

·45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr 180 185 190

Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp

Asn Val Ala Val Lys Glu Ser Ser Asn Ala 245 250

<210> 36

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

 <221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB40m5;p GenBank #AF349989

<400> 36

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
Met Gly Lys Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

tct ttt tgg tta gtt act gct gct cta tta gca tct act gta ttt ttc

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe

35

40

45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

gta tcg ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

_		_			gag Glu			_	_			_		_		288
	_				aca Thr											336
					aca Thr											384
					gtt Val											432
					tgg Trp 150											480
					gaa Glu											528
					gct Ala											576
					tgg Trp											624
tac Tyr	cta Leu 210	atg Met	ggt Gly	gac Asp	ggt Gly	gga Gly 215	tca Ser	gct Ala	ctt Leu	aac Asn	tta Leu 220	aac Asn	ctt Leu	atc Ile	tat Tyr	672
		_	_		gtt Val 230		_									720
	-	_	_		gaa Glu											750

<210> 37

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 37

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu 100 ' 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 140

Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp 145 150 155 160

```
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys
                165
                                     170
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
            180
                                 185
                                                      190
Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
                             200
                                                  205
        195
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
                                             220
    210
                         215
Asn Leu Ala Asp Phe Val Asn Lys Asn Leu Phe Gly Leu Ile Ile Trp
                                                              240
                                         235
                     230
225
Asn Val Ala Val Lys Glu Ser Ser Asn Ala
                                     250
                245
<210>
       38
<211>
       750
<212>
       DNA
<213>
       Naturally occurring gamma proteobacterium
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<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB40m12; GenBank # AF34999

<400> 38

_											att Ile					48
											gat Asp					96
											tct Ser					144
											aaa Lys 60					192
											cat His					240
											act Thr					288
											tgt Cys					336
											tta Leu					384
	_				_	_					tac Tyr 140					432
											ggg Gly					480
											gga Gly					528
aat Asn	act Thr	gca Ala	agt Ser 180	cct Pro	gct Ala	gtg Val	caa Gln	tca Ser 185	gct Ala	tac Tyr	aac Asn	aca Thr	atg Met 190	atg Met	tat Tyr	576

		-					tat Tyr 205		6	524
_	_						aac Asn		6	672
	_	_	_	_			tta Leu		 7	720
_	_	_	-	tct Ser	_				7	750

<210> 39

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 39

Met Gly Lys Leu Leu Arg Ile Leu Gly Ser Val Ile Ala Leu Pro Thr 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr 180 185 190

Ile Ile Ile Val Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala 245 250

<210> 40

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<222>
          (1)..(750)
          Proteorhodopsin variant from pcr clone MB100m5; GenBank #AF349991
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   <400> 40
                                                                          48
   atq qqt aaa tta tta ctq ata tta ggt agt gtt att gca ctt cct aca
   Met Gly Lys Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
10
                                                            15
   ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt
                                                                          96
   Phe Ala Ala Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
               20
Ш
                                                                         144
   tet ttt tgg tta gtt aca get get eta tta gea tet act gta ttt tte
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
U
                                                    45
           35
                               40
C
                                                                         192
   ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act
   Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
       50
                           55
   gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg
                                                                         240
   Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
                       70
                                           75
                                                                80
   65
                                                                         288
   aga gga gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac
   Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
                                                                         336
   att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta
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Naturally occurring gamma proteobacterium

750

DNA

CDS

100

<211>

<212>

<213>

<220>

<221>

110

384

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu

att ctt gct gct gca act aat gtt gcc ggc tca tta ttt aag aaa ctt

105

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Ile	Leu	Ala 115	Ala	Ala	Thr	Asn	Val 120	Ala	Gly	Ser	Leu	Phe 125	Lys	Lys	Leu	
	_				_	_					tac Tyr 140	-	_	-		432
		_	_								gly ggg					480
											gga Gly					528
											aac Asn					576
		_									ggt Gly					624
											tta Leu 220					672
		_	_		_		_				ggt Gly					720
	_	gct Ala	_		_											750

<210> 41

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 41

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala

```
Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
          195
  Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
      210
                           215
                                               220
  Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
                                           235
                                                                240
  225
                       230
  Asn Val Ala Val Lys Glu Ser Ser Asn Ala
                  245
                                       250
  <210>
         42
  <211>
         750
<212>
         DNA
         Naturally occurring gamma proteobacterium
  <213>
  <220>
<221> CDS
  <222>
         (1)..(750)
Proteorhodopsin variant from pcr clone MB100m7; GenBank #AF349992
  <223>
  <400> 42
                                                                          48
  atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca
  Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
                                                            15
  1
                   5
                                       10
                                                                          96
  ttt gct gca ggt ggt gac ctt gat gct agt gat tac act ggt gtt
  Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
                                                        30
                                   25
               20
                                                                         144
  tot ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc
  Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
          35
                               40
                                                   45
```

	_	_	_	-	aga Arg						192
_				_	act Thr 70						240
					gaa Glu						288
					aca Thr						336
					act Thr						384
					gtt Val						432
					tgg Trp 150						480
					gaa Glu						528
					tcg Ser						576
					tgg Trp						624
					ggt Gly						672
					gtt Val 230						720

aat gct gct gtt aaa gaa tct tct aat gct Asn Ala Ala Val Lys Glu Ser Ser Asn Ala 245 250

<210> 43

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 43

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr 1 5 10 15

Phe Ala Ala Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu 115 120 125

```
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140
```

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys 165 170 175

Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala 180 185 190

Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp 225 230 230 235

Asn Ala Ala Val Lys Glu Ser Ser Asn Ala 245 250

<210> 44

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<223> Proteorhodopsin variant from pcr clone MB100m9; GenBank #AF349993

	<400)> 4	14															
	_				tta Leu 5	_				_								48
					ggt Gly													96
					gtt Val												:	144
		_	-	-	gat Asp												:	192
L L. L. 4.	_				gtt Val												:	240
					att Ile 85												:	288
		_			cta Leu		_										;	336
			_	_	gca Ala			_										384
					ctt Leu												4	432
					gca Ala												•	480
	gta	tac	atg	att	tat	gaa	cta	tgg	gct	gga	gaa	gga	aaa	tct	gca	tgt	!	528

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp

Asn V	al	Ala	Val	Lys 245	Glu	Ser	Ser	Asn	Ala 250								
<210>	4	16															
<211>	7	50															
<212>	· I	NA															
<213>	N	Jatur	ally	000	urri	.ng g	gamma	a pro	teok	pacte	eriun	n					
<220>																	
<221>		DS															
<222>	. ((1)	(750))													
<223>	· E	rote	orho	dops	sin v	varia	ant i	Erom	pcr	clor	ne ME	3100r	n10;	GenI	Bank	#AF34999	
			tta	tta	ctg	ata	tta	ggt	agt	gtt	att	gca	ctt	cct	aca	48	
Met G				Leu													
	ct	aca	aat		aat	gac	ctt	gat		agt.	gat.	tac	act	aat	att	96	
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□ Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
□ 50 55 60
□
□
□

口 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 切 85 90 95 口

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Val Gly Cys Leu Ala Trp 145 150 155 160

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  Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
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  Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
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  Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
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												gca Ala					1	44
												aaa Lys 60					1	L92
												cat His					2	240
												aca Thr					2	288
												gtt Val					3	336
Harman Harman												tta Leu					3	384
												ttt Phe 140					4	132
												ggt Gly					4	180
												ggt Gly					Ę	528
												aat Asn					Ę	576
	att Ile	att Ile	gtt Val 195	att Ile	gga Gly	tgg Trp	gca Ala	att Ile 200	tat Tyr	cct Pro	gct Ala	gga Gly	tat Tyr 205	gct Ala	gct Ala	ggt Gly	(524

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Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu 100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu 115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala 130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Leu Gly Met Ala Gly Trp 145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu His Met Gly Glu Gly Lys Ala Ala Val 165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Lys 180 185 190

Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly 195 200 205

Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile 210 215 220

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                                                                          96
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  Phe Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
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  Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
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  Phe Val Glu Arg Asp Gln Val Ser Ala Glu Trp Lys Thr Ser Leu Thr
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  Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
                   85
                                                            95
                                                                         336
  att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta
  Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
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                                   105
                                                        110
                                                                         384
  att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt
   Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
                                                   125
           115
                               120
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  cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct
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Leu	Ala 130	Gly	Ser	Leu	Val	Met 135	Leu	Gly	Ala	Gly	Phe 140	Ala	Gly	Glu	Ala	
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		atg Met														528
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Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu 115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala 130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp 145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val 165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met 180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
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  Phe Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
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                                                       30
              20
  tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt
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  Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
                                                   45
          35
                               40
                                                                         192
  ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act
  Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
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                           55
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WHT.

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_		_			gac Asp			_								288
					act Thr											336
					aca Thr											384
					gta Val											432
		_		_	tgg Trp 150											480
Leu	Tyr	Met	Ile	Tyr 165	gag Glu	Leu	Tyr	Met	Gly 170	Glu	Gly	Lys	Ala	Ala 175	Val	528
agt Ser	act Thr	gca Ala	agt Ser 180	cct Pro	gct Ala	gtt Val	aac Asn	tct Ser 185	gca Ala	tac Tyr	aac Asn	gca Ala	atg Met 190	atg Met	atg Met	576
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Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met

65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu 100 105 110

Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu 115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala 130 135 140

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Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
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  Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
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                                                            175
                   165
  Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met
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                                   185
                                                        190
  Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
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                                                    205
           195
  Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
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                                                220
  Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
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							act Thr											288
							gtt Val											336
-							agt Ser											384
							atg Met 135											432
							cct Pro											480
							cta Leu											528
	agt	act	gca	agt	cct	gct	gtt	aac	tct	gca	tac	aac	gca	atg	atg	atg	٠	576

	Ser	Thr	Ala	Ser 180	Pro	Ala	Val	Asn	Ser 185	Ala	Tyr	Asn	Ala	Met 190	Met	Met	
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	Ser	Phe	Trp 35	Leu	Val	Thr	Ala	Gly 40	Met	Leu	Ala	Ala	Thr 45	Val	Phe	Phe	
	Phe	Val 50	Glu	Arg	Asp	Gln	Val 55	Ser	Ala	Lys	Trp	Lys 60	Thr	Ser	Leu	Thr	

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Ser Ala Gly Glu Ala Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala

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  65
                       70
                                           75
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  Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
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                                                            95
                                                                         336
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														atg Met 190		576
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Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr 85 90 95

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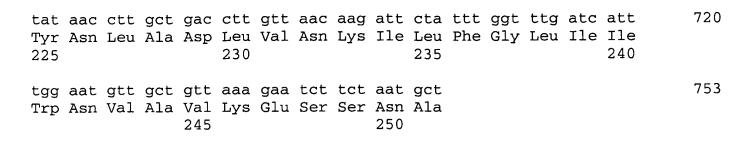
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Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp 145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val 165 170 175

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                                    185
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                               200
                                                    205
   Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
       210
                           215
   Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
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                                                            15
   1
                   5
                                        10
                                                                          96
   ttt gct gct gct ggc gat cta gat ata agt gat act gtt ggt gtt
   Phe Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
                                   25
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               20
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				aca Thr								144
_	_	_	-	caa Gln	_	_	_	_				192
				act Thr 70								240
				gac Asp								288
				act Thr								336
				aca Thr								384
				gta Val								432
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<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacteria

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Phe Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val 20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe 35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu 100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu 115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala 130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp 145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val 165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met 180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly 195 200 205

Tyr Leu Met Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile 210 215 220

Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile 225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala 245 250

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<212> DNA

<213> Naturally occurring gamma proteobacteria





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<223> Proteorhodopsin variant from pcr clone PalE1;GenBank# AF350001

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		tgg Trp 35		-												1	44
	_	gaa Glu				_	_									1	92
		ggt Gly														2	40
_		gtt Val			_		~ ~	_				_		_		2	88
	_	tgg Trp				_					_	_				3	36
		gct Ala 115	_	_		_	_	_								3	84
	-	ggt Gly			_	_										4	32
gga	tta	gct	cct	gta	tta	cct	gct	ttc	att	att	ggt	atg	gct	gga	tgg	4	80

	1y 45	Leu	Ala	Pro	Val	Leu 150	Pro	Ala	Phe	Ile	Ile 155	Gly	Met	Ala	Gly	Trp 160	
			_			gag Glu			_		_		_	_	_	_	528
	_		-	_		gct Ala	_			_			_	_	_	_	576
			_	_		tgg Trp	_				_			_	_		624
			_			gaa Glu											672
\mathbf{T}				_	_	ttt Phe 230	-		_					_			720
						aaa Lys											753
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<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacteria

<400> 61

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Phe Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val 20 25 30



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Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met 65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Val Val Glu Phe Tyr Leu 100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu 115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala 130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp 145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val 165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Pro Ala Tyr Asn Ala Met Met Met 180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile 210 215 220



Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile 225 230 235 240

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				gat Asp						288
				act Thr						336
	_		_	aca Thr						384
				gta Val						432
				tta Leu 150						480
				gag Glu						528
				gct Ala						576
				tgg Trp						624
	_	-		gac Asp						672
				ttt Phe 230						720
				aaa Lys						753

<210> 63

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 63

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Phe Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val 20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe 35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met 65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu 100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu 115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala 130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp 145 150 155 160 Leu Tyr Met Ile Tyr Glu Leu His Met Gly Glu Gly Lys Ala Ala Val 165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Lys 180 185 190

Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile 210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile 225 230 235 240

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					ggc Gly											96
					aca Thr											144
	_	_	_	_	caa Gln	_	_	_	_							192
					act Thr 70											240
					gat Asp											288
					act Thr											336
		_	-	_	aca Thr	-	_	_	-						ctt Leu	384
Leu		Gly	Ser	Leu	gta Val	Met	Leu	Gly	Ala	Gly	Phe	Ala				432
					tta Leu 150											480
		_			gag Glu											528
_					gct Ala											576
att	att	gtt	gtt	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggt	624

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly 195 200 205	
tac cta atg ggt ggc gaa ggc gta tac gct tca aac tta aac ctt ata Tyr Leu Met Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile 210 215 220	2
tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile 225 230 235 240)
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Arg Gly Val Trp ,Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala 245 250

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D9847513 OSO101

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DOBHYSIB . OSOIOI

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APPENDIX

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APPENDIX

COELTET OSCIOI

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ogetysis oscioi

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COSHIST OSOIOI

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COCHYSIE, OSCIOI

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COSTILL OSCIOL

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APPENDIX

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APPENDIX A

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COMFIGURE CECHOL

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CORHYGLE OSCIOL

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